Emmanuelle Genin

List of Publications by Year
in descending order

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		61945	38368
184	10,136	43	95
papers	citations	h-index	g-index

206	206	206	15960
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	NGS mismapping confounds the clinical interpretation of the PRSS1 p.Ala16Val (c.47C>T) variant in chronic pancreatitis. Gut, 2022, 71, 841-842.	6.1	8
2	Heritability: What's the point? What is it not for? A human genetics perspective. Genetica, 2022, 150, 199-208.	0.5	4
3	Functionally deficient TRPV6 variants contribute to hereditary and familial chronic pancreatitis. Human Mutation, 2022, 43, 228-239.	1.1	7
4	RAVAQ: An integrative pipeline from quality control to regionâ€based rare variant association analysis. Genetic Epidemiology, 2022, , .	0.6	2
5	Moment estimators of relatedness from low-depth whole-genome sequencing data. BMC Bioinformatics, 2022, 23, .	1.2	1
6	A <scp>BBS1 SVA</scp> F retrotransposon insertion is a frequent cause of <scp>Bardetâ€Biedl</scp> syndrome. Clinical Genetics, 2021, 99, 318-324.	1.0	21
7	Extension of SKAT to multi-category phenotypes through a geometrical interpretation. European Journal of Human Genetics, 2021, 29, 736-744.	1.4	4
8	The reversion variant (p.Arg90Leu) at the evolutionarily adaptive p.Arg90 site in CELA3B predisposes to chronic pancreatitis. Human Mutation, 2021, 42, 385-391.	1.1	6
9	Scale and Scope of Gene-Alcohol Interactions in Chronic Pancreatitis: A Systematic Review. Genes, 2021, 12, 471.	1.0	9
10	CFTR Cooperative Cis-Regulatory Elements in Intestinal Cells. International Journal of Molecular Sciences, 2021, 22, 2599.	1.8	3
11	Whole exome sequencing, a hypothesis-free approach to investigate recurrent early miscarriage. Reproductive BioMedicine Online, 2021, 42, 789-798.	1.1	3
12	Evaluation of saliva as a source of accurate wholeâ€genome and microbiome sequencing data. Genetic Epidemiology, 2021, 45, 537-548.	0.6	2
13	SLITRK2, an X-linked modifier of the age at onset in C9orf72 frontotemporal lobar degeneration. Brain, 2021, 144, 2798-2811.	3.7	7
14	Chronic Pancreatitis: The True Pathogenic Culprit within the SPINK1 N34S-Containing Haplotype Is No Longer at Large. Genes, 2021, 12, 1683.	1.0	5
15	Endâ€Truncated <scp>LAMB1</scp> Causes a Hippocampal Memory Defect and a Leukoencephalopathy. Annals of Neurology, 2021, 90, 962-975.	2.8	5
16	The Interplay between the Unfolded Protein Response, Inflammation and Infection in Cystic Fibrosis. Cells, 2021, 10, 2980.	1.8	12
17	Phenotypic Differences Between Polygenic and Monogenic Hypobetalipoproteinemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, e63-e71.	1.1	12
18	Missing heritability of complex diseases: case solved?. Human Genetics, 2020, 139, 103-113.	1.8	109

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19	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
20	Role of the Common PRSS1-PRSS2 Haplotype in Alcoholic and Non-Alcoholic Chronic Pancreatitis: Meta- and Re-Analyses. Genes, 2020, 11, 1349.	1.0	14
21	Privacy-Preserving Genome-Wide Association Study for Rare Mutations - A Secure FrameWork for Externalized Statistical Analysis. IEEE Access, 2020, 8, 112515-112529.	2.6	2
22	Rare variant association testing in the non-coding genome. Human Genetics, 2020, 139, 1345-1362.	1.8	21
23	The genetic history of France. European Journal of Human Genetics, 2020, 28, 853-865.	1.4	15
24	Contribution of rare and predicted pathogenic gene variants to childhood-onset lupus: a large, genetic panel analysis of British and French cohorts. Lancet Rheumatology, The, 2020, 2, e99-e109.	2.2	38
25	49th European Mathematical Genetics Meeting (EMGM) 2021. Human Heredity, 2020, 85, 69-100.	0.4	1
26	Secure Collapsing Method Based on Fully Homomorphic Encryption. Studies in Health Technology and Informatics, 2020, 270, 412-416.	0.2	0
27	Blood transcriptomic biomarker as a surrogate of ischemic brain gene expression. Annals of Clinical and Translational Neurology, 2019, 6, 1681-1695.	1.7	17
28	Rare variant association testing for multicategory phenotype. Genetic Epidemiology, 2019, 43, 646-656.	0.6	9
29	Sensitive Skin: Lessons From Transcriptomic Studies. Frontiers in Medicine, 2019, 6, 115.	1.2	9
30	RRAD mutation causes electrical and cytoskeletal defects in cardiomyocytes derived from a familial case of Brugada syndrome. European Heart Journal, 2019, 40, 3081-3094.	1.0	48
31	Secure Multilayer Perceptron Based on Homomorphic Encryption. Lecture Notes in Computer Science, 2019, , 322-336.	1.0	9
32	Genetics and postsurgical neuropathic pain. European Journal of Anaesthesiology, 2019, 36, 342-350.	0.7	5
33	Principals about principal components in statistical genetics. Briefings in Bioinformatics, 2019, 20, 2200-2216.	3.2	24
34	GEMPROT: visualization of the impact on the protein of the genetic variants found on each haplotype. Bioinformatics, 2019, 35, 2492-2494.	1.8	0
35	Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. Brain, 2019, 142, 35-49.	3.7	44
36	High prevalence of congenital deafness on Reunion Island is due to a founder variant of LHFPL5. Clinical Genetics, 2019, 95, 177-181.	1.0	7

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37	Rare Coding Variants in ANGPTL6 Are Associated with Familial Forms of Intracranial Aneurysm. American Journal of Human Genetics, 2018, 102, 133-141.	2.6	37
38	MACARON: a python framework to identify and re-annotate multi-base affected codons in whole genome/exome sequence data. Bioinformatics, 2018, 34, 3396-3398.	1.8	5
39	Identification of potential genetic risk factors for bipolar disorder by whole-exome sequencing. Translational Psychiatry, 2018, 8, 268.	2.4	16
40	Association of modifiers and other genetic factors explain Marfan syndrome clinical variability. European Journal of Human Genetics, 2018, 26, 1759-1772.	1.4	73
41	Estimating the age of p.(Phe508del) with family studies of geographically distinct European populations and the early spread of cystic fibrosis. European Journal of Human Genetics, 2018, 26, 1832-1839.	1.4	45
42	Rare RNF213 variants in the C-terminal region encompassing the RING-finger domain are associated with moyamoya angiopathy in Caucasians. European Journal of Human Genetics, 2017, 25, 995-1003.	1.4	77
43	Identification of a functional enhancer variant within the chronic pancreatitisâ€associatedSPINK1c.101A>G (p.Asn34Ser)â€containing haplotype. Human Mutation, 2017, 38, 1014-1024.	1.1	18
44	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. Molecular Psychiatry, 2017, 22, 1119-1125.	4.1	57
45	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. Neurobiology of Aging, 2017, 59, 220.e1-220.e9.	1.5	116
46	Factors influencing the age at onset in familial frontotemporal lobar dementia. Neurology: Genetics, 2017, 3, e203.	0.9	8
47	In silico search for modifier genes associated with pancreatic and liver disease in Cystic Fibrosis. PLoS ONE, 2017, 12, e0173822.	1.1	14
48	DoEstRare: A statistical test to identify local enrichments in rare genomic variants associated with disease. PLoS ONE, 2017, 12, e0179364.	1.1	7
49	ABCA7 rare variants and Alzheimer disease risk. Neurology, 2016, 86, 2134-2137.	1.5	63
50	Biallelic Variants in UBA5 Reveal that Disruption of the UFM1 Cascade Can Result in Early-Onset Encephalopathy. American Journal of Human Genetics, 2016, 99, 695-703.	2.6	87
51	Accuracy of heritability estimations in presence of hidden population stratification. Scientific Reports, 2016, 6, 26471.	1.6	19
52	DCTN4 as a modifier of chronicPseudomonas aeruginosainfection in cystic fibrosis. Clinical Respiratory Journal, 2016, 10, 777-783.	0.6	10
53	Highlighting the impact of cascade carrier testing in cystic fibrosis families. Journal of Cystic Fibrosis, 2016, 15, 452-459.	0.3	8
54	Relationship inference from the genetic data on parents or offspring: A comparative study. Theoretical Population Biology, 2016, 107, 31-38.	0.5	1

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55	Multiple imputation for competing risks regression with interval-censored data. Journal of Statistical Computation and Simulation, 2016, 86, 2217-2228.	0.7	14
56	SORL1 rare variants: a major risk factor for familial early-onset Alzheimerâ€™s disease. Molecular Psychiatry, 2016, 21, 831-836.	4.1	96
57	Revisiting the Polygenic Additive Liability Model through the Example of Diabetes Mellitus. Human Heredity, 2015, 80, 171-177.	0.4	14
58	High level of inbreeding in final phase of 1000 Genomes Project. Scientific Reports, 2015, 5, 17453.	1.6	68
59	The Missing Heritability Paradigm: A Dramatic Resurgence of the GIGO Syndrome in Genetics. Human Heredity, 2015, 79, 1-4.	0.4	13
60	Genome-wide association study identifies TF as a significant modifier gene of iron metabolism in HFE hemochromatosis. Journal of Hepatology, 2015, 62, 664-672.	1.8	62
61	Confirmation of a founder effect in a Northern European population of a new Î²-globin variant: HBB:c.23_26dup (codons 8/9 (+AGAA)). European Journal of Human Genetics, 2015, 23, 1158-1164.	1.4	1
62	Integration of Omics Data in Genetic Epidemiology. Human Heredity, 2015, 79, 109-110.	0.4	4
63	Identification of a functionalPRSS1promoter variant in linkage disequilibrium with the chronic pancreatitis-protecting rs10273639. Gut, 2015, 64, 1837-1838.	6.1	35
64	Population Stratification of Rare Variants. , 2015, , 227-237.		2
65	Poor Survival in Rheumatoid Arthritis Associated with Bronchiectasis: A Family-Based Cohort Study. PLoS ONE, 2014, 9, e110066.	1.1	30
66	Haploinsufficiency of Dmxl2, Encoding a Synaptic Protein, Causes Infertility Associated with a Loss of GnRH Neurons in Mouse. PLoS Biology, 2014, 12, e1001952.	2.6	66
67	FSuite: exploiting inbreeding in dense SNP chip and exome data. Bioinformatics, 2014, 30, 1940-1941.	1.8	30
68	Gene expression profile in hereditary transthyretin amyloidosis: differences in targeted and source organs. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2014, 21, 113-119.	1.4	13
69	A Homogenizing Process of Selection Has Maintained an â€œUltra-Slowâ€•Acetylation NAT2 Variant in Humans. Human Biology, 2014, 86, 185.	0.4	19
70	HLA-A*31:01 and different types of carbamazepine-induced severe cutaneous adverse reactions: an international study and meta-analysis. Pharmacogenomics Journal, 2014, 14, 281-288.	0.9	199
71	How important are rare variants in common disease?. Briefings in Functional Genomics, 2014, 13, 353-361.	1.3	76
72	Inbreeding Coefficient Estimation with Dense SNP Data: Comparison of Strategies and Application to HapMap III. Human Heredity, 2014, 77, 49-62.	0.4	46

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73	Epistatic Interaction between BANK1 and BLK in Rheumatoid Arthritis: Results from a Large Trans-Ethnic Meta-Analysis. PLoS ONE, 2013, 8, e61044.	1.1	24
74	Advantage of Using Allele-Specific Copy Numbers When Testing for Association in Regions with Common Copy Number Variants. PLoS ONE, 2013, 8, e75350.	1.1	6
75	Molecular Reclassification of Crohnâ€™s Disease: A Cautionary Note on Population Stratification. PLoS ONE, 2013, 8, e77720.	1.1	5
76	High imatinib dose overcomes insufficient response associated with ABCG2 haplotype in chronic myelogenous leukemia patients. Oncotarget, 2013, 4, 1582-1591.	0.8	26
77	Mutation in a primate-conserved retrotransposon reveals a noncoding RNA as a mediator of infantile encephalopathy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4980-4985.	3.3	58
78	Lung cancer and DNA repair genes: multilevel association analysis from the International Lung Cancer Consortium. Carcinogenesis, 2012, 33, 1059-1064.	1.3	41
79	Could Inbred Cases Identified in GWAS Data Succeed in Detecting Rare Recessive Variants Where Affected Sib-Pairs Have Failed?. Human Heredity, 2012, 74, 142-152.	0.4	8
80	Comparative Power of Familyâ€Based Association Strategies to Detect Diseaseâ€Causing Variants Under Twoâ€Locus Models. Genetic Epidemiology, 2012, 36, 848-855.	0.6	4
81	Genome-wide CNV analysis replicates the association between GSTM1 deletion and bladder cancer: a support for using continuous measurement from SNP-array data. BMC Genomics, 2012, 13, 326.	1.2	14
82	Positive Selection in the Chromosome 16 VKORC1 Genomic Region Has Contributed to the Variability of Anticoagulant Response in Humans. PLoS ONE, 2012, 7, e53049.	1.1	9
83	Rare and Low Frequency Variant Stratification in the UK Population: Description and Impact on Association Tests. PLoS ONE, 2012, 7, e46519.	1.1	23
84	No replication of genetic association between candidate polymorphisms and Alzheimer's disease. Neurobiology of Aging, 2011, 32, 1443-1451.	1.5	57
85	Consanguinity around the world: what do the genomic data of the HGDP-CEPH diversity panel tell us?. European Journal of Human Genetics, 2011, 19, 583-587.	1.4	52
86	APOE and Alzheimer disease: a major gene with semi-dominant inheritance. Molecular Psychiatry, 2011, 16, 903-907.	4.1	529
87	Interleukin-36â€“Receptor Antagonist Deficiency and Generalized Pustular Psoriasis. New England Journal of Medicine, 2011, 365, 620-628.	13.9	836
88	Genome-wide association study of Stevens-Johnson Syndrome and Toxic Epidermal Necrolysis in Europe. Orphanet Journal of Rare Diseases, 2011, 6, 52.	1.2	99
89	Autism risk assessment in siblings of affected children using sex-specific genetic scores. Molecular Autism, 2011, 2, 17.	2.6	19
90	Assessment of copy number variation using the Illumina Infinium 1M SNP-array: a comparison of methodological approaches in the Spanish Bladder Cancer/EPICURO study. Human Mutation, 2011, 32, 240-248.	1.1	57

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91	Mutations of the cystic fibrosis gene in patients with bronchiectasis associated with rheumatoid arthritis. Annals of the Rheumatic Diseases, 2011, 70, 653-659.	0.5	34
92	Genetic Association and Gene-Environment Interaction: A New Method for Overcoming the Lack of Exposure Information in Controls. American Journal of Epidemiology, 2011, 173, 225-235.	1.6	23
93	Genomeâ€scan for bipolar disorder with sibâ€pair families in the Sardinian population: A new susceptibility locus on chromosome 1p22â€“p21?. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1200-1208.	1.1	8
94	On the use of sibling recurrence risks to select environmental factors liable to interact with genetic risk factors. European Journal of Human Genetics, 2010, 18, 88-94.	1.4	4
95	Trente ans d'Ã©tude de la maladie de Rendu-Osler en FranceÂ: dÃ©mographie historique, gÃ©nÃ©tique des populations et biologie molÃ©culaire. Population, 2009, Vol. 64, 305-325.	0.1	3
96	The very low penetrance of cystic fibrosis for the R117H mutation: a reappraisal for genetic counselling and newborn screening. Journal of Medical Genetics, 2009, 46, 752-758.	1.5	106
97	Impaired performance of FDRâ€based strategies in wholeâ€genome association studies when SNPs are excluded prior to the analysis. Genetic Epidemiology, 2009, 33, 45-53.	0.6	17
98	On the use of phylogenyâ€based tests to detect association between quantitative traits and haplotypes. Genetic Epidemiology, 2009, 33, 729-739.	0.6	7
99	Familial Mediterranean Fever In Lebanon: Founder Effects For DifferentMEFVMutations. Annals of Human Genetics, 2008, 72, 41-47.	0.3	23
100	Identifying modifier genes of monogenic disease: strategies and difficulties. Human Genetics, 2008, 124, 357-368.	1.8	103
101	Investigation of the fine structure of European populations with applications to disease association studies. European Journal of Human Genetics, 2008, 16, 1413-1429.	1.4	147
102	Hereditary hemorrhagic telangiectasia: evidence for regional founder effects of ACVRL1 mutations in French and Italian patients. European Journal of Human Genetics, 2008, 16, 742-749.	1.4	35
103	HLA-DRB1*15 allele influences the later course of relapsing remitting multiple sclerosis. Genes and Immunity, 2008, 9, 570-574.	2.2	23
104	On the Origin of the Transthyretin Val30Met Familial Amyloid Polyneuropathy. Annals of Human Genetics, 2008, 72, 478-484.	0.3	52
105	Founder Effect and Estimation of the Age of the c.892C>T (p.Arg298Cys) Mutation in LMNA Associated to Charcotâ€Marieâ€Tooth Subtype CMT2B1 in Families from North Western Africa. Annals of Human Genetics, 2008, 72, 590-597.	0.3	27
106	Estimating the age of CFTR mutations predominantly found in Brittany (Western France). Journal of Cystic Fibrosis, 2008, 7, 168-173.	0.3	21
107	Cystic fibrosis carrier frequency and estimated prevalence of the disease in Morocco. Journal of Cystic Fibrosis, 2008, 7, 440-443.	0.3	16
108	The CHRNE 1293insG founder mutation is a frequent cause of congenital myasthenia in North Africa. Neurology, 2008, 71, 1967-1972.	1.5	30

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109	A Weighted-Holm Procedure Accounting for Allele Frequencies in Genomewide Association Studies. Genetics, 2008, 180, 697-702.	1.2	6
110	Selecting Predictive Markers for Pharmacogenetic Traits: Tagging vs. Data-Mining Approaches. Human Heredity, 2008, 66, 10-18.	0.4	4
111	Evidence for a Locus in 1p31 Region Specifically Linked to the Co-Morbidity of Asthma and Allergic Rhinitis in the EGEA Study. Human Heredity, 2007, 63, 162-167.	0.4	13
112	Dealing with missing phase and missing data in phylogeny-based analysis. BMC Proceedings, 2007, 1, S22.	1.8	2
113	Efficiency of multiple imputation to test for association in the presence of missing data. BMC Proceedings, 2007, 1, S24.	1.8	2
114	Pleiotropic Effects of CEP290 (NPHP6) Mutations Extend to Meckel Syndrome. American Journal of Human Genetics, 2007, 81, 170-179.	2.6	248
115	A mixture model approach to multiple testing for the genetic analysis of gene expression. BMC Proceedings, 2007, 1, S141.	1.8	5
116	Power comparison of different methods to detect genetic effects and gene-environment interactions. BMC Proceedings, 2007, 1, S74.	1.8	3
117	Dealing with Missing Data in Family-Based Association Studies: A Multiple Imputation Approach. Human Heredity, 2007, 63, 229-238.	0.4	25
118	Spectrum ofMKS1andMKS3mutations in Meckel syndrome: a genotype-phenotype correlation. Human Mutation, 2007, 28, 523-524.	1.1	92
119	Are genome-wide association studies all that we need to dissect the genetic component of complex human diseases?. European Journal of Human Genetics, 2007, 15, 260-263.	1.4	25
120	Using Genomic Inbreeding Coefficient Estimates for Homozygosity Mapping of Rare Recessive Traits: Application to Taybi-Linder Syndrome. American Journal of Human Genetics, 2006, 79, 62-66.	2.6	48
121	Selection of SNP subsets for association studies in candidate genes: comparison of the power of different strategies to detect single disease susceptibility locus effects. BMC Genetics, 2006, 7, 20.	2.7	10
122	Clustering of haplotypes based on phylogeny: how good a strategy for association testing?. European Journal of Human Genetics, 2006, 14, 202-206.	1.4	8
123	Clinical and molecular genetic features of ARC syndrome. Human Genetics, 2006, 120, 396-409.	1.8	118
124	ALTree: association detection and localization of susceptibility sites using haplotype phylogenetic trees. Bioinformatics, 2006, 22, 1402-1403.	1.8	6
125	Further Evidence That the UGT1A1*28 Allele Is Not Associated with Coronary Heart Disease: The ECTIM Study. Clinical Chemistry, 2006, 52, 2313-2314.	1.5	35
126	Complex trait mapping in isolated populations: Are specific statistical methods required?. European Journal of Human Genetics, 2005, 13, 698-706.	1.4	28

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127	On the use of haplotype phylogeny to detect disease susceptibility loci. BMC Genetics, 2005, 6, 24.	2.7	40
128	Impact of the diagnosis definition on linkage detection. BMC Genetics, 2005, 6, S140.	2.7	1
129	ABCA2 is a strong genetic risk factor for early-onset Alzheimer's disease. Neurobiology of Disease, 2005, 18, 119-125.	2.1	109
130	Estimating the age of rare disease mutations: the example of Triple-A syndrome. Journal of Medical Genetics, 2004, 41, 445-449.	1.5	112
131	Coincidence of two genetic forms of Charcotâ€“Marieâ€“Tooth disease in a single family. Neurology, 2004, 63, 1527-1529.	1.5	38
132	Handling missing values in population data: consequences for maximum likelihood estimation of haplotype frequencies. European Journal of Human Genetics, 2004, 12, 805-812.	1.4	33
133	Investigation of seven proposed regions of linkage in multiple sclerosis: an American and French collaborative study. Neurogenetics, 2004, 5, 45-48.	0.7	23
134	Genetic analysis of multiple sclerosis in Europeans: French data. Journal of Neuroimmunology, 2003, 143, 74-78.	1.1	13
135	Does accounting for gene-environment (GÃ—E) interaction increase the power to detect the effect of a gene in a multifactorial disease?. Genetic Epidemiology, 2003, 24, 200-207.	0.6	22
136	Testing linkage and Gene Ã— Environment interaction: Comparison of different affected sib-pair methods. Genetic Epidemiology, 2003, 25, 73-79.	0.6	9
137	Genetic interaction ofCTLA-4 with HLA-DR15 in multiple sclerosis patients. Annals of Neurology, 2003, 54, 119-122.	2.8	46
138	Intercellular adhesion molecule-1: a protective haplotype against multiple sclerosis. Genes and Immunity, 2003, 4, 518-523.	2.2	30
139	A risk for early-onset Alzheimer's disease associated with the APBB1 gene (FE65) intron 13 polymorphism. Neuroscience Letters, 2003, 342, 5-8.	1.0	14
140	No replication of the association between the Nicastrin gene and familial early-onset Alzheimer's disease. Neuroscience Letters, 2003, 353, 153-155.	1.0	10
141	Estimation of the Inbreeding Coefficient through Use of Genomic Data. American Journal of Human Genetics, 2003, 73, 516-523.	2.6	221
142	Hypogonadotropic hypogonadism due to loss of function of the KiSS1-derived peptide receptor GPR54. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10972-10976.	3.3	2,094
143	Deleterious Genetic Influence of CX3CR1 Genotypes on HIV-1 Disease Progression. Journal of Acquired Immune Deficiency Syndromes (1999), 2003, 32, 335-337.	0.9	30
144	Association Studies in Candidate Genes: Strategies to Select SNPs to Be Tested. Human Heredity, 2003, 56, 151-159.	0.4	25

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145	Absence of Association of Thrombophilia Polymorphisms with Intrauterine Growth Restriction. New England Journal of Medicine, 2002, 347, 19-25.	13.9	248
146	Inherited Interleukin-12 Deficiency: IL12B Genotype and Clinical Phenotype of 13 Patients from Six Kindreds. American Journal of Human Genetics, 2002, 70, 336-348.	2.6	265
147	Properties of the transmission-disequilibrium test in the presence of inbreeding. Genetic Epidemiology, 2002, 22, 116-127.	0.6	5
148	Impact of parental relationships in maximum lod score affected sib-pair method. Genetic Epidemiology, 2002, 23, 413-425.	0.6	25
149	Missing data in haplotype analysis: a study on the MILC method. Annals of Human Genetics, 2002, 66, 99-108.	0.3	16
150	Comparison of family based haplotype methods using intragenic SNPs in candidate genes. European Journal of Human Genetics, 2002, 10, 313-319.	1.4	2
151	Linkage of one gene for familial glucocorticoid deficiency type 2 (FGD2) to chromosome 8q and further evidence of heterogeneity. Human Genetics, 2002, 111, 428-434.	1.8	27
152	Accurate power approximations for chi2-tests in case-control association studies of complex disease genes. Annals of Human Genetics, 2002, 66, 307-21.	0.3	8
153	INTERLEUKIN 1 GENE CLUSTER POLYMORPHISMS IN MULTIPLEX FAMILIES WITH SPONDYLARTHROPATHIES. Cytokine, 2001, 13, 98-103.	1.4	38
154	Use of Closely Related Affected Individuals for the Genetic Study of Complex Diseases in Founder Populations. American Journal of Human Genetics, 2001, 68, 154-159.	2.6	41
155	Maximum Identity Length Contrast: A Powerful Method For Susceptibility Gene Detection in Isolated Populations. Genetic Epidemiology, 2001, 21, S560-4.	0.6	15
156	Selection of Single Nucleotide Polymorphisms for Association Studies in Candidate Genes. Genetic Epidemiology, 2001, 21, S614-S619.	0.6	5
157	Cladistic Analysis of Haplotypes as an Attempt to Detect Disease Susceptibility. Genetic Epidemiology, 2001, 21, S602-7.	0.6	3
158	Investigation of a Candidate Gene, Environment, and GÃ—E Interaction Using Caseâ€Control and Caseâ€Parent Study Designs. Genetic Epidemiology, 2001, 21, S843-8.	0.6	1
159	Determination of polychlorodibenzo-p-dioxins and polychlorodibenzofurans by gas chromatography/tandem mass spectrometry and gas chromatography/triple mass spectrometry in a quadrupole ion trap. Journal of Mass Spectrometry, 2001, 36, 546-554.	0.7	8
160	Modeling of HLA class II susceptibility to Type I diabetes reveals an effect associated with DPB1. Genetic Epidemiology, 2001, 21, 212-223.	0.6	30
161	Evidence for digenic inheritance in a family with both febrile convulsions and temporal lobe epilepsy implicating chromosomes 18qter and 1q25-q31. Annals of Neurology, 2001, 49, 786-792.	2.8	92
162	Modeling the HLA component in rheumatoid arthritis: Sensitivity to DRB1 allele frequencies. Genetic Epidemiology, 2000, 19, 422-428.	0.6	7

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163	Application of liquid chromatography with mass spectrometry combined with photodiode array detection and tandem mass spectrometry for monitoring pesticides in surface waters. Journal of Chromatography A, 2000, 879, 51-71.	1.8	157
164	Search for multifactorial disease susceptibility genes in founder populations. Annals of Human Genetics, 2000, 64, 255-265.	0.3	75
165	A robust test for assortative mating. European Journal of Human Genetics, 2000, 8, 119-124.	1.4	36
166	Rapid Progression to AIDS in HIV+ Individuals with a Structural Variant of the Chemokine Receptor CX3CR1. Science, 2000, 287, 2274-2277.	6.0	305
167	Molecular basis of variant pseudo-Hurler polydystrophy (mucolipidosis IIIC). Journal of Clinical Investigation, 2000, 105, 673-681.	3.9	171
168	Detection and modeling of disease susceptibility locus effects: How much can be learned from contrast of populations?. Genetic Epidemiology, 1999, 17, S569-S574.	0.6	0
169	Detection of polymorphism in the RING3 gene by high-throughput fluorescent SSCP analysis. Immunogenetics, 1999, 49, 256-265.	1.2	8
170	Modelling the major histocompatibility complex susceptibility to RA using the MASC method. , 1998, 15, 419-430.		24
171	Reply to Weeks and Sinsheimer. American Journal of Human Genetics, 1998, 62, 731-736.	2.6	7
172	On the Probability of Identity States in Permutable Populations: Reply to Cannings. American Journal of Human Genetics, 1998, 62, 728-729.	2.6	7
173	A Gene for Meckel Syndrome Maps to Chromosome 11q13. American Journal of Human Genetics, 1998, 63, 1095-1101.	2.6	95
174	Exclusion of the Adrenocorticotropin (ACTH) Receptor (MC2R) Locus in Some Families with ACTH Resistance but No Mutations of the MC2R Coding Sequence (Familial Glucocorticoid Deficiency Type) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	23
175	Optimization of genome search strategies for homozygosity mapping: influence of marker spacing on power and threshold criteria for identification of candidate regions. Annals of Human Genetics, 1998, 62, 419-429.	0.3	17
176	Exclusion of the Adrenocorticotropin (ACTH) Receptor (MC2R) Locus in Some Families with ACTH Resistance but No Mutations of the MC2R Coding Sequence (Familial Glucocorticoid Deficiency Type) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	7
177	Genetic heterogeneity of Meckel syndrome.. Journal of Medical Genetics, 1997, 34, 1003-1006.	1.5	18
178	Quantitative analysis of C60 fullerene in blood and tissues by high-performance liquid chromatography with photodiode-array and mass spectrometric detection. Biomedical Applications, 1997, 696, 153-159.	1.7	51
179	Information provided by pairs of distantly affected relatives to search for genes involved in rare autosomal dominant diseases. Annals of Human Genetics, 1997, 61, 25-34.	0.3	1
180	Caution in the interpretation of MLS. Genetic Epidemiology, 1997, 14, 1079-1083.	0.6	7

#	Article	IF	Citations
181	Heterogeneity of marker allele frequencies hinders interpretation of linkage analysis: Illustration on chromosome 18 markers. Genetic Epidemiology, 1997, 14, 669-674.	0.6	6
182	Genetic susceptibility to rheumatoid arthritis: Study of HLA-DR and TNF loci using the masc method. Human Immunology, 1996, 47, 77.	1.2	0
183	Lack of association of angiotensin Iâ€converting enzyme gene polymorphism and premature myocardial infarction in Mauritian Indians. Clinical Genetics, 1996, 50, 551-554.	1.0	8
184	Posterior probability of linkage and maximal lod score. Annals of Human Genetics, 1995, 59, 123-132.	0.3	16